In the Specification:

Please replace the paragraph beginning at page 3, line 19, with the following:

A1

--Figure 1A shows the polynucleotide sequence of the VHL/E US28 coding sequence (SEQ ID NO:3) and Figure 1B shows the amino acid sequence for the corresponding VHL/E US28 polypeptide (SEQ ID NO:4). The extracellular domain is underlined.--

Please replace the paragraph beginning at page 3, line 22, with the following:

A2

--Figure 2 is a sequence comparison of the amino acid sequences for human US28 (AD169) (upper sequence; SEQ ID NO:48), rhesus US28.1 (second sequence; SEQ ID NO:6), rhesus US28.2 (third sequence; SEQ ID NO:8), rhesus US28.3 (fourth sequence; SEQ ID NO:10), rhesus US28.4 (fifth sequence; SEQ ID NO:12) and rhesus US28.5 (bottom sequence; SEQ ID NO:14). Regions of sequence similarity are indicated in the boxed regions as determined using the sequence comparision program, SeqVu, from the Garvan Institute, Sydney, Australia. Shaded regions correspond to regions of similar hydrophilicity or hydrophobicity as determined by the SeqVu program.--

Please replace the paragraph beginning at page 3, line 29, with the following:

A3

--Figure 3 is a sequence comparison of the amino acid sequences for human UL78 [strain AD169 (Genebank Accession # X17403, see, e.g., Chee et al., 1990, *Curr. Top. Microbiol. Immunol.* 154:125-169] (upper sequence; SEQ ID NO:16) and rhesus UL78 (lower sequence; SEQ ID NO:18). Regions of sequence similarity are indicated in the boxed regions as determined using the comparision program SeqVu,

A3

from the Garvan Institute, Sydney, Australia, with shaded regions corresponding to regions of similar hydrophilicity or hydrophobicity as determined by the same program.--

Please replace the paragraph beginning at page 4, line 3, with the following:

A4

--Figure 4 is a sequence comparison of the amino acid sequences for human UL33 [Genebank Accession # X17403; see, e.g., Chee et al., 1990, *Curr. Top. Microbiol. Immunol.* 154:125-169] (upper sequence; SEQ ID NO:20), human UL33 spliced (second sequence; SEQ ID NO:22), rhesus UL33 (third sequence; SEQ ID NO:24) and rhesus UL33 spliced (lower sequence; SEQ ID NO:26). Regions of sequence similarity are indicated in the boxed regions as determined using the comparision program SeqVu, from the Garvan Institute, Sydney, Australia; regions of similar hydrophilicity or hydrophobicity as determined by the same program are shaded.--

Please replace the paragraph (Table 4) beginning at page 27, line 7, with the following:

--Table 4: Primer sequences for amplifying rhUS28 homologs.

rhUS28 Homolog	Primer Sequence (Upper Strand)	SEQ ID NO:	Primer Sequence (Lower Strand)	SEQ ID NO:
rhUS28.1	TATGAATAACACATCTTGCAACTTC	28	CACACAGACCACATGTAC	29
rhUS28.2	ATTCAACATGACCAACGCCGG	30	GCATTTCCGTGGATTCG	31
rhUS28.3	CATGACCAACACTAAC	32	GAGTCTTTTGTGAGCC	33
rhUS28.4	TATGAATTCGAGCCAGCAC	34	GTACGCGACTAAGACAGAG	35
rhUS28.5	AAAGATGACTACCACCAC	36	ATAACCTAGCACCTCCCC	37
rhUL78	CTGAAACCATGATTACGG	38	CACGCAGCACAAGAGCAC	39
rhUL33	CATGACCAATCTTTACTC	40	GTGTCGCCACTCCTACCC	41
rhUL33 spliced	AAGTTAGTGATGGCAGTC	42	GTATGTAAACCCGTGGAG	43

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Please replace the paragraph beginning at page 35, line 11, with the following:

--Typically, the antisense polynucleotides used in the methods comprise an antisense sequence of typically at least about 10 contiguous nucleotides, in other instances at least 12 or 14 contiguous nucleotides, and in still other instances up to about 100 contiguous nucleotides that specifically hybridize to a sequence from a mRNA encoding US28 or a US28 homolog in the target organism. Thus, in the treatment of infections caused by human strains of CMV, appropriate polynucleotides sequences can be prepared based upon the nucleotide sequence for human US28 as set forth in SEQ ID NO:3 (FIG. 1A) and for human UL33 (SEQ ID NO:19), human UL33 spliced (SEQ ID NO:21) and human UL78 (SEQ ID NO:15). Likewise, in the treatment of infections

A6

caused by rhesus strains, appropriate polynucleotides can be prepared based upon the nucleotide sequences for the various rhesus US28 homologs as shown in SEQ ID NOS:5, 7, 9, 11, 13, 17, 23 and 25.--

Please replace the paragraph beginning at page 36, line 9, with the following:

A7

--Ribozymes are also useful for inhibiting US28 or US28 homolog activity in an animal. Useful ribozymes can comprise 5'- and 3'-terminal sequences complementary to the US28 mRNA or US28 homolog mRNA and can be engineered by one of skill on the basis of the US28 mRNA sequence (see, e.g., SEQ ID NO:3; see FIG. 1A) and US28 homolog sequences disclosed herein (SEQ ID NOS:5, 7, 9, 11, 13, 17, 23 and 25). Ribozymes that can be utilized in the treatment methods include those having characteristics of group I intron ribozymes (Cech, 1995, *Biotechnology* 13:323) and others of hammerhead ribozymes (Edgington, 1992, *Biotechnology* 10:256).--

Please replace the paragraph beginning at page 37, line 5, with the following:

A8

--Antibodies are an example of one type of agent that can be used to inhibit binding between a chemokine and US28 or a US28 homolog. Such inhibition can be achieved, for example, through steric hindrance. Typically, the antibody specifically binds an epitope on the extracellular region of US28 (e.g., SEQ ID NO:4; see FIG. 1B) or one of the US28 homologs. Thus, certain treatments involve administering an antibody that specifically binds to human UL33 (SEQ ID NO:20), human UL33 spliced (SEQ ID NO:22) or human UL78 (SEQ ID NO:16). Other treatment methods involve administering an antibody that specifically binds to one of the rhesus US28 homologs (i.e., SEQ ID NOS:6, 8, 10, 12, 14, 18, 24 and 26).--

Please replace the paragraph beginning at page 38, line 33, with the following:

A9

--The vaccines are generally designed to include CMV or some portion of the virion in which US28 or US28 homolog has been disabled such that US28 or US28 protein is either not produced or is produced in inactive form. In some instances, this means that the segment of the genome encoding US28 or US28 homolog has been completely or substantially removed, either chemically, enzymatically or via recombination. Specific segments, or at least portions thereof, that can be removed for HCMV include those regions of the genome corresponding to US28 (SEQ ID NOS:1 and 3), UL33 (SEQ ID NO:19), UL33 spliced (SEQ ID NO:21) and UL78 (SEQ ID NO:15). For rhCMV, segments, or portions thereof, that can be removed include SEQ ID NOS:5, 7, 9, 11, 13, 17, 23 and 25.--

Please replace the paragraph beginning at page 43, line 24, with the following:

A10

--A list of the sequence identifiers for the nucleotide sequences of the open reading frames encoding the rhesus US 28 homologs and the corresponding amino acid sequences are summarized in Table 3 *supra*. The actual nucleotide and amino acid sequences of the rhesus US28 homologs are shown in SEQ ID NOS:5, 7, 9, 11, 13, 17, 23 and 25 (nucleotide sequences) and SEQ ID NOS:6, 8, 10, 12, 14, 18, 24 and 26 (amino acid sequences).--

Please insert the accompanying paper copy of the Sequence Listing, page numbers 1 to 33, at the end of the application.